

sequences and biallelic markers thereof
 JOURNAL Patent: WO 0100803-A 4 04-JAN-2001;
 GENSET (FR)

FEATURES
 source Location/Qualifiers

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 /db_xref="taxon:9606"
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 exon
 1442. 1498
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 Best Local Similarity 100.0%: Pred. No. 2.6e-27;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 CAAATCTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 120
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 DB 312 CAAATCTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 371
 QY 121 C 121
 DB 372 C 372

RESULT 2
 AX469879 5381 bp DNA linear PAT 09-AUG-2002
 LOCUS
 DEFINITION Sequence 4 from Patent WO02053734.
 ACCESSION AX469879
 VERSION AX469879.1 GI:22205152
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1

AUTHORS Bouguetel, L., Duclert, A., Clusel, C., Dumas, M.E., Yen-Potin, F.,
 Denison, B., Blahin, B., Bour, B., Ebbers, R., and Salter, Cld. L.
 TITLE Methods and compositions for inhibiting neoplastic cell growth
 JOURNAL Patent: WO 02053734-A 4 11-JUL-2002;
 GENSET SA (FR)

FEATURES
 source Location/Qualifiers

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 /note="3' regulatory region"
 BASE COUNT 1104 a 1434 c 1709 g 1132 t 2 others
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Query Match 99.7%: Score 120.6; DB 6; Length 5381;
 Best Local Similarity 100.0%: Pred. No. 2.6e-27;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTTGGGCTTGCCTCTCCAGAGCCCTCGCAGTCGAGTTCAGCTTTTCCTCATGGGG 60
 |||||||
 DB 252 GCATTTGGGCTTGCCTCTCCAGAGCCCTCGCAGTCGAGTTCAGCTTTTCCTCATGGGG 311
 QY 61 CAAATCTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 120
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 DB 312 CAAATCTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 371
 QY 121 C 121
 DB 372 C 372

RESULT 3
 AX063464 81001 bp DNA linear PAT 24-JAN-2001
 LOCUS
 DEFINITION Sequence 1 from Patent WO0100803.
 ACCESSION AX063464
 VERSION AX063464.1 GI:12541234
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 81001)

AUTHORS Yen, F., Denison, B., Bour, B., Bihain, B., Bougueleret, L., Duclet, A. and dumas milne Edwards, J.B.
 TITLE Apolipoprotein a-iv-related protein: polypeptide, polynucleotide sequences and biallelic markers thereof
 JOURNAL Patent: WO 0100803-A 1 04-JAN-2001;
 GENSET (FR)

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 Best local Similarity 100.0% ; Pred. No. 2.5e-27 ;
 Matches 121 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
 QY 1 GCATTGGGCTTGCTCTCTCAGAGGCCCTGCGAGTGAAGTTCAGCTTTTCTTCATGGG 60
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 QY 61 CAATCTTACTTTCGCTCCAGTTCCTGGGGCTGAGATCCCTGGCCAGATGCTCTTGC 120
 Db 12340 CAATCTTACTTTCGCTCCAGTTCCTGGGGCTGAGATCCCTGGCCAGATGCTCTTGC 12399
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 Db 12400 c 12400

RESULT 4
 LOCUS AX469876 81001 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 1 from Patent WO02053734.
 ACCESSION AX469876
 VERSION AX469876.1 GI:22205149
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Bougueleret, L., Duclet, A., Clusel, C., Dumas, M.E., Yen-Potin, F.,
 Denison, B., Bihain, B., Bour, B., Ebberts-Reed, D., and Sater-Cid, L.
 TITLE Methods and compositions for inhibiting neoplastic cell growth
 JOURNAL Patent: WO 02053734-A 1 11-JUL-2002;
 GENSET SA (FR)
 FEATURES
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BASE COUNT      20291 a 17705 c 19080 g 23919 t      6 others
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Query Match      99.7% ; Score 120.6 ; DB 6 ; Length 81001 ;
Best Local Similarity 100.0% ; Pred. No. 2.5e-27 ;
Matches 121 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
QY      1 GCATTGGGCTTGCTGCTCCAGAGCGCCGCGAGTGGAGTTCCTTCATGAGG 60
Db      12280 GCATTGGGCTTGCTGCTCCAGAGCGCCGCGAGTGGAGTTCCTTCATGAGG 12339
QY      61 CAATCTYACTTTCGCTCCAGATTCCTGGGCTCAGATCCCTGAGCCAGATGCTTTC 120
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QY      121 C 121
Db      12400 C 12400

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RESULT 5
AP001480/c      115027 bp      DNA      linear      HTC 30-MAY-2000
LOCUS      Homo sapiens chromosome 11 clone CTC-227C10 map 11q, WORKING DRAFT
DEFINITION
ACCESSION      AP001480
VERSION      AP001480.2 GI:8117338
KEYWORDS      HMG; HMG5_Phasel; HMG5_DRAFT.
SOURCE      Homo sapiens DNA, clone CTC-227C10.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 115027)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 115,027 genomic DNA of 11q
Published only in Database (2000)
2 (bases 1 to 115027)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
TITLE      Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
Kitsaslo Univ., 1-15-1 Kitsaslo, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7288164.
COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humdrat11
Center clone name: CTC-227C10
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 107728 bases at least Q40
Consensus quality: 110501 bases at least Q30
Consensus quality: 11810 bases at least Q20
Insert size: 113327; sum-of-contigs
Quality coverage: 6.70x in Q20 bases; sum-of-contigs

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NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and the order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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1 15681 contig of 15681 bp in length
15782 30275 contig of 14494 bp in length
30376 40528 contig of 10153 bp in length
40629 50205 contig of 9577 bp in length
50306 59617 contig of 9312 bp in length
59718 66750 contig of 7033 bp in length
66851 73847 contig of 6997 bp in length
73948 79644 contig of 5909 bp in length
79745 85653 contig of 5488 bp in length
85754 91241 contig of 5078 bp in length
91342 96419 contig of 4179 bp in length
96520 100644 contig of 2125 bp in length
100745 102923 contig of 2927 bp in length
103024 105950 contig of 2888 bp in length
106051 108938 contig of 2539 bp in length
109039 111577 contig of 1810 bp in length
111678 113487 contig of 1440 bp in length
113588 115027 contig of 1440 bp in length

Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 15681: contig of 15681 bp in length
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91342 96419: contig of 5078 bp in length
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102924 103023: gap of 100 bp
103024 105950: contig of 2927 bp in length
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106051 108938: contig of 2888 bp in length
108939 109038: gap of 100 bp
109039 111577: contig of 2539 bp in length
111578 111677: gap of 100 bp
111678 113487: contig of 1810 bp in length
113488 113587: gap of 100 bp
113588 115027: contig of 1440 bp in length.

FEATURES
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Best Local Similarity 99.28; Pred. No. 2; Se-27;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTTGGCGTCTGCTCCAGAGGCCCTCCAGCTTCACTTTCCTTCATGCGG 60
DB 55154 GCATTTGGCGTCTGCTCCAGAGGCCCTCCAGCTTCACTTTCCTTCATGCGG 55095
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QY 121 C 121
DB 55034 C 55034

RESULT 6
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LOCUS Homo sapiens chromosome 11 clone CTC-270C21 map 11g, WORKING DRAFT
DEFINITION SEQUENCE: 29 unordered pieces.
ACCESSION AP001481
VERSION AP001481.2 GI:8117339
KEYWORDS HTG; HTGS; PHASE1; HTGS; DRAFT.
SOURCE Homo sapiens DNA, clone: CTC-270C21.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 175582)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.
TITLE Homo sapiens 175,582 genomic DNA of 11g
JOURNAL Published only in Database (2000)
REFERENCE 2 (bases 1 to 175582)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.
TITLE Direct Submission

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JOURNAL

Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Kitasato Univ., 1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555, Japan (E-mail:hattori@sc.riken.go.jp, URL: http://hqp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) On May 30, 2000 this sequence version replaced g1:7288175.

COMMENT

Center: RIKEN Genomic Sciences Center(GSC)

Center code: RIKEN

Web site: http://hqp.gsc.riken.go.jp/

Contact: hattori@sc.riken.go.jp

Project Information

Center project name: HumPrat11

Center clone name: CTC-270C21

Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 162298 bases at least Q40

Consensus quality: 169842 bases at least Q30

Insert size: 172782; sum-of-contrigs

Quality coverage: 4.96x in Q20 bases; sum-of-contrigs

NOTE: This is a 'working draft' sequence. It currently consists of 29 contrigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contrigs are represented as runs 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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1 16627 contrig of 16627 bp in length
30721 30620 contrig of 13893 bp in length
42540 42439 contrig of 11719 bp in length
53522 53421 contrig of 10882 bp in length
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77020 76919 contrig of 12071 bp in length
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176919 176818 contrig of 1798 bp in length
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FEATURES

Source

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* 64749 64848: gap of 100 bp
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* 77020 85523: contrig of 8504 bp in length
* 85524 85623: gap of 100 bp
* 85624 94708: contrig of 9085 bp in length
* 94709 94808: gap of 100 bp
* 94809 104076: contrig of 9268 bp in length
* 104077 104176: gap of 100 bp
* 104177 112629: contrig of 8453 bp in length
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* 112730 119309: contrig of 6580 bp in length
* 119310 119409: gap of 100 bp
* 119410 126696: contrig of 7287 bp in length
* 126697 126796: gap of 100 bp
* 126797 132422: contrig of 5626 bp in length
* 132423 132522: gap of 100 bp
* 132523 137920: contrig of 5398 bp in length
* 137921 138020: gap of 100 bp
* 138021 142190: contrig of 4170 bp in length
* 142191 142290: gap of 100 bp
* 142291 145283: contrig of 2993 bp in length
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* 148551 148650: gap of 100 bp
* 148651 151425: contrig of 2775 bp in length
* 151426 151525: gap of 100 bp
* 151526 155432: contrig of 3907 bp in length
* 155433 155532: gap of 100 bp
* 155533 158018: contrig of 2486 bp in length
* 158019 158118: gap of 100 bp
* 158119 160661: contrig of 2543 bp in length
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* 163243 163342: gap of 100 bp
* 163343 165254: contrig of 1912 bp in length
* 165255 165354: gap of 100 bp
* 165355 167624: contrig of 2270 bp in length
* 167625 167724: gap of 100 bp
* 167725 169398: contrig of 1674 bp in length
* 169399 169498: gap of 100 bp
* 169499 171146: contrig of 1648 bp in length
* 171147 171246: gap of 100 bp
* 171247 173044: contrig of 1798 bp in length
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* 173145 174332: contrig of 1188 bp in length
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Source

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 in multiple unrelated t(11;22) families
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 AUTHORS Hu, P. and Roe, B.A.
 TITLE Direct Submission

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JOURNAL Submitted (02-JUN-1999) Department of Chemistry And Biochemistry,  

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,  

OK 73019, USA
REFERENCE 3 (bases 1 to 188971)
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          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /map="11q23"
          /clone="442e11 from RPC111 library"
          /note="442e11 was originally named b1030"
BASE COUNT 53091 a 44581 c 42653 g 48646 t
ORIGIN

Query Match      99.7%; Score 120.6; DB 9; Length 188971;
Best Local Similarity 99.2%; Pred. No. 2.5e-27;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGGGCTGCTCTCTCCAGAGCCCTCGAGTGGAGTTTCAGCTTTTCATGAGG 60
    |||||||
Db 78721 GCATTGGGCTGCTCTCTCCAGAGCCCTCGAGTGGAGTTTCAGCTTTTCATGAGG 78662

QY 61 CAAATCTYACTTTCGCTCCAGTCTCGGGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 120
    |||||||
Db 78661 CAAATCTYACTTTCGCTCCAGTCTCGGGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 78602

QY 121 C 121
Db 78601 C 78601

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RESULT 8
 AC074203
 LOCUS Homo sapiens chromosome 22q11 clone cos4, complete sequence.
 DEFINITION Homo sapiens chromosome 22q11 Cosmid cos4
 ACCESSION AC074203
 VERSION AC074203.3 GI:9625348
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 42479)
 AUTHORS Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Homo sapiens Chromosome 22q11 Cosmid cos4
 JOURNAL Unpublished
 REMARK This clone is a chimeric cosmid from a patient with t(11;22)
 translocation and it is from the derivative chromosome 11. There
 are sequences from both chromosome 11 and 22 in this cosmid
 2 (bases 1 to 42479)
 REFERENCE 2 (bases 1 to 42479)
 AUTHORS Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (18-JUL-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA
 3 (bases 1 to 42479)
 Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (03-AUG-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 4 (bases 1 to 42479)
 Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (13-OCT-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 COMMENT On Aug 1, 2000 this sequence version replaced gi:9441829.
 FEATURES
 SOURCE Location/Qualifiers
 1..42479
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="22q11"
 /clone="cos4"
 BASE COUNT 11501 a 9314 c 9563 g 12101 t
 ORIGIN
 Query Match 98.3%; Score 119; DB 9; Length 42479;
 Best Local Similarity 98.3%; Pred. No. 8.1e-27;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATGCGG 60
 |||||||
 DB 31388 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATGCGG 31447
 |||||||
 QY 61 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTCG 120
 |||||||
 DB 31448 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTCG 31507
 |||||||
 QY 121 C 121
 DB 31508 C 31508

RESULT 9
 AC113242 181412 bp DNA linear HTG 27-FEB-2002
 LOCUS Pan troglodytes clone RP43-68H20, WORKING DRAFT SEQUENCE, 4
 DEFINITION AC113242
 AC113242
 AC113242.1 GI:18958669
 HTG: HTGS_PHASE1: HTGS_DRAFT.
 VERSION
 KEYWORDS
 SOURCE Pan t:oglodites.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 1 (bases 1 to 181412)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Unpublished
 2 (bases 1 to 181412)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and
 Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2002) Berkeley PGA, Lawrence Berkeley National
 Laboratory, 1 Cyclotron rd., Berkeley, CA 94720, United States of
 America
 COMMENT Draft Sequence Produced by Berkeley PGA
 pga.lbl.gov
 Center Code: PGABERK.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
 1 2162: contig of 2162 bp in length
 * 2163 2262: gap of unknown length
 * 2263 5105: contig of 2843 bp in length
 * 5205 5205: gap of unknown length
 * 5206 47902: contig of 42697 bp in length
 * 47903 48002: gap of unknown length
 * 48003 181412: contig of 133410 bp in length.
 FEATURES
 SOURCE Location/Qualifiers
 1..181412
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="RP43-68H20"
 BASE COUNT 45821 a 41573 c 43021 g 50687 t 310 others
 ORIGIN
 Query Match 97.0%; Score 117.4; DB 2; Length 181412;
 Best Local Similarity 97.5%; Pred. No. 2.5e-26;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATGCGG 60
 |||||||
 DB 102546 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATGCGG 102605
 |||||||
 QY 61 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTCG 120
 |||||||
 DB 102606 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTCG 102665
 |||||||
 QY 121 C 121
 DB 102666 C 102666

RESULT 10
 AC118574 191656 bp DNA linear HTG 19-APR-2002
 LOCUS Lemur catta clone LB2-277C3, WORKING DRAFT SEQUENCE, 10 unordered
 DEFINITION AC118574
 AC118574
 AC118574.1 GI:20198538
 HTG: HTGS_PHASE1: HTGS_DRAFT.
 VERSION
 KEYWORDS
 SOURCE Lemur catta.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
 1 (bases 1 to 191656)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and
 Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Unpublished
 2 (bases 1 to 191656)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and
 Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (19-APR-2002) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 COMMENT Draft Sequence Produced by Berkeley PGA
 web site: http://pga.lbl.gov
 Center Code: PGABERK
 Additional Information:
 Comparative analysis and ordering by homology are available
 here: http://pga.lbl.gov/cgi-bin/search/cvcdtype=navalue-APO1
 Funding agent: Programs for Genomic Applications (NHLBI)
 Contact: 'Jody Schwartz' jschwartz@lbl.gov
 Summary Statistics
 Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.

Db 206197 GTTTTCCCCTCCCTGGGAGGGCCGGGGGCTGTGACTTCAGTCTTTTGGACACGGGGGGAAGGCT 206256
 QY 69 ACTTTCGCTCCAGTTCCTGGGGCTCAGATGCCCTTGGCCAGAT 111
 Db 206257 TCTCTCTCTCCCTTCTCTTCGGGTCCAGATGCCCTGTACTGCT 206299

RESULT 13			
AX323765			
LOCUS	5377 bp	DNA	
DEFINITION	Sequence 253 from Patent WO0192565.	linear	PAT 07-JAN-2002

REFERENCE	1
AUTHORS	Olek, A., Piepenbrock, C. and Berlitz, K.
TITLE	Diagnosis of diseases associated with dna transcription
JOURNAL	Patent: WO 0192565-A 253 06-DEC-2001;
FEATURES	Epigenomics Ag (DE)
	location/Qualifiers
	1 5375

Query Match	34.0%	Score 41.2;	DB 6;	Length 5377;
Best Local Similarity	68.8%	Pred. No. 0.024;		
Matches	55;	Mismatches	24;	Indels 0; Gaps 0;
	Conservative			

RESULT 14	AC126842	185476 bp	DNA	linear	HTG 10-JUL-2007
LOCUS	AC126842				
DEFINITION	Rattus norvegicus clone CH230-10C10, *** SPOUNCM:MG IN PROGRESS				
ACCESSION	AC126842				
VERSION	AC126842.1	GI:21722906			
KEYWORDS	HTG; HTGS_PHASE1.				
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 185476)
AUTHORS	Morley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (10-Jul-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	----- Genome Center

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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.bncs.bcm.tmc.edu/docs/genbank\_draft\_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 69 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1428: contig of 1428 bp in length
*
* 1429 1528: gap of unknown length
*
* 1529 2823: contig of 1295 bp in length
*
* 2824 2923: gap of unknown length
*
* 2924 4456: contig of 1533 bp in length
*
* 4457 4557: gap of unknown length
*
* 4557 5693: contig of 1137 bp in length
*
* 5694 5793: gap of unknown length
*
* 5794 6982: contig of 1189 bp in length
*
* 6983 7083: gap of unknown length
*
* 7083 8311: contig of 1229 bp in length
*
* 8312 8411: gap of unknown length
*
* 8412 9949: contig of 1537 bp in length
*
* 9949 10048: gap of unknown length

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```

* 10049 11110: contig of 1062 bp in length
* 11111 11210: gap of unknown length
* 11211 12358: contig of 1148 bp in length
* 12359 12458: gap of unknown length
* 12459 13851: contig of 1393 bp in length
* 13852 13951: gap of unknown length
* 13952 15147: contig of 1196 bp in length
* 15148 15247: gap of unknown length
* 15248 16349: contig of 1102 bp in length
* 16350 16449: gap of unknown length
* 16450 17680: contig of 1231 bp in length
* 17681 17780: gap of unknown length
* 17781 19551: contig of 1771 bp in length
* 19552 19651: gap of unknown length
* 19652 20914: contig of 1263 bp in length
* 20915 21014: gap of unknown length
* 21015 22689: contig of 1675 bp in length
* 22690 22789: gap of unknown length
* 22790 24844: contig of 2055 bp in length
* 24845 24944: gap of unknown length
* 24945 26501: contig of 1557 bp in length
* 26502 28343: contig of 1742 bp in length
* 28344 28443: gap of unknown length
* 28444 30014: contig of 1571 bp in length
* 30015 31432: contig of 1318 bp in length
* 31433 31532: gap of unknown length
* 31533 33678: contig of 2346 bp in length
* 33679 33978: gap of unknown length
* 33979 35999: contig of 2021 bp in length
* 36000 36099: gap of unknown length
* 36100 37879: contig of 1780 bp in length
* 37880 37979: gap of unknown length
* 37980 40493: contig of 2514 bp in length
* 40494 40593: gap of unknown length
* 40594 43007: contig of 2414 bp in length
* 43008 43107: gap of unknown length
* 43108 45425: contig of 2318 bp in length
* 45426 45525: gap of unknown length
* 45526 47696: contig of 2171 bp in length
* 47697 47796: gap of unknown length
* 47797 49161: contig of 1365 bp in length
* 49162 49261: gap of unknown length
* 49262 51962: contig of 2701 bp in length
* 51963 52062: gap of unknown length
* 52063 54983: contig of 2921 bp in length
* 54984 55083: gap of unknown length
* 55084 57601: contig of 2518 bp in length
* 57602 57701: gap of unknown length
* 57702 59300: contig of 1599 bp in length
* 59301 59400: gap of unknown length
* 59401 61170: contig of 1770 bp in length
* 61171 61270: gap of unknown length
* 61271 63401: contig of 2131 bp in length
* 63402 63501: gap of unknown length
* 63502 66845: contig of 3344 bp in length
* 66846 66945: gap of unknown length
* 66946 68915: contig of 1970 bp in length
* 68916 69015: gap of unknown length
* 69016 71351: contig of 2336 bp in length
* 71352 71451: gap of unknown length
* 71452 73280: contig of 1829 bp in length
* 73281 73380: gap of unknown length
* 73381 76521: contig of 3141 bp in length
* 76522 76621: gap of unknown length
* 76622 79787: contig of 3166 bp in length
* 79788 79887: gap of unknown length
* 79888 83405: contig of 3518 bp in length
* 83406 83505: gap of unknown length
* 83506 85714: contig of 2209 bp in length
* 85715 85814: gap of unknown length
* 85815 87631: contig of 1817 bp in length

```

```

* 87632 87731: gap of unknown length
* 87732 89911: contig of 2180 bp in length
* 89912 90011: gap of unknown length
* 90012 91542: contig of 1531 bp in length
* 91543 91642: gap of unknown length
* 91643 94772: contig of 3130 bp in length
* 94773 94872: gap of unknown length
* 94873 96801: contig of 2029 bp in length
* 96802 96902: gap of unknown length
* 96903 99943: contig of 2942 bp in length
* 99944 100043: gap of unknown length
* 100044 102874: contig of 2831 bp in length
* 102875 102974: gap of unknown length
* 102975 106306: contig of 3332 bp in length
* 106307 106407: gap of unknown length
* 106408 110217: contig of 3811 bp in length
* 110218 110317: gap of unknown length
* 110318 113446: contig of 3029 bp in length
* 113447 113446: gap of unknown length
* 113447 115933: contig of 2487 bp in length
* 115934 116033: gap of unknown length
* 116034 120425: contig of 4392 bp in length
* 120426 120525: gap of unknown length
* 120526 123358: contig of 2833 bp in length
* 123359 123458: gap of unknown length
* 123459 126381: contig of 2923 bp in length
* 126382 126481: gap of unknown length

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Query Match 29.3%; Score 35.4; DB 2; Length 185476;
Best Local Similarity 66.2%; Pred. No. 1.5;
Matches 51; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 26 GCCCTGCGAGTGAATTCCTTCCTCATGGGCAATCTGCTCCAGCTCC 85
Db 81542 GCTCTTCACAGCAATCCAGTTTCCATTTGGCTGAAAACGTACTGATCCAGTTCC 81601
Qy 86 TGGGGCTCAGAGTCCCT 102
Db 81602 AGGAGATCTGAACCT 81618

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```

RESULT 15
AC025626 154696 bp DNA linear HTG 28-MAY-2000
LOCUS Homo sapiens clone RP11-216B13, WORKING DRAFT SEQUENCE, 35
DEFINITION Homo sapiens clone RP11-216B13, WORKING DRAFT SEQUENCE, 35
ACCESSION AC025626
VERSION AC025626.3 GI:8099800
KEYWORDS HTG, HTGS_PHASE1, HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 154696)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bede,F.,
Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choege,Y., Colanero,M., Collins,S.,
Collimore,A., Cooke,P., Deatellano,K., Dewar,K., Diaz,J.S.,
Dodg,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galgan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howard,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
Melidim,J., Menus,L., Mihova,T., Miranda,C., Mienga,Y., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,

```

TITLE
JOURNAL
COMMENT

Pisanti, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teftaye, S., Theodore, J., Tirrell, A., Travers, M., Trifilillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA
On May 28, 2000 this sequence version replaced g1:7657088.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://f.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIDR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L5807

Center clone name: 216.B.13

Sequencing vector: M13: M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 135951 bases at least Q40

Consensus quality: 145629 bases at least Q30

Consensus quality: 148984 bases at least Q20

Insert size: 149000; agarose-fp

Insert size: 151296; sum-of-contigs

Quality coverage: 3.7 in Q20 bases; agarose-fp

Quality coverage: 3.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1      1088: contig of 1088 bp in length
*      1089 1188: gap of 100 bp
*      1189 2246: contig of 1058 bp in length
*      2247 2346: gap of 100 bp
*      2347 3505: contig of 1159 bp in length
*      3506 3605: gap of 100 bp
*      3606 4777: contig of 1172 bp in length
*      4778 4877: gap of 100 bp
*      4878 6634: contig of 1757 bp in length
*      6635 6734: gap of 100 bp
*      6735 8097: contig of 1363 bp in length
*      8098 8197: gap of 100 bp
*      8198 10306: contig of 2109 bp in length
*      10307 10406: gap of 100 bp
*      10407 12406: contig of 2000 bp in length
*      12407 12506: gap of 100 bp
*      12507 14219: contig of 1713 bp in length
*      14220 14319: gap of 100 bp
*      14320 16072: contig of 1753 bp in length
*      16073 16172: gap of 100 bp
*      16173 17723: contig of 1551 bp in length
*      17724 17823: gap of 100 bp
*      17824 19608: contig of 1785 bp in length
*      19609 19708: gap of 100 bp
*      19709 22007: contig of 2299 bp in length
*      22008 22107: gap of 100 bp
*      22108 23950: contig of 1843 bp in length
*      23951 24050: gap of 100 bp
*      24051 26881: contig of 2831 bp in length
*      26882 26981: gap of 100 bp
*      26982 29772: contig of 2791 bp in length
*      29773 29872: gap of 100 bp

```

FEATURES

source

```

*      29873 32507: contig of 2635 bp in length
*      32608 32607: gap of 100 bp
*      32608 36314: contig of 3707 bp in length
*      36315 36414: gap of 100 bp
*      36415 38838: contig of 2824 bp in length
*      38839 38938: gap of 100 bp
*      38939 42279: contig of 3341 bp in length
*      42280 42379: gap of 100 bp
*      42380 44940: contig of 2561 bp in length
*      44941 45040: gap of 100 bp
*      45041 48483: contig of 3443 bp in length
*      48484 48583: gap of 100 bp
*      48584 52752: contig of 4169 bp in length
*      52753 52852: gap of 100 bp
*      52853 57771: contig of 4919 bp in length
*      57772 57871: gap of 100 bp
*      57872 61962: contig of 4091 bp in length
*      61963 62062: gap of 100 bp
*      62063 65728: contig of 3666 bp in length
*      65729 65828: gap of 100 bp
*      65829 69752: contig of 3924 bp in length
*      69753 69852: gap of 100 bp
*      69853 76487: contig of 6635 bp in length
*      76488 76587: gap of 100 bp
*      76588 84995: contig of 8408 bp in length
*      84996 85095: gap of 100 bp
*      85096 91863: contig of 6768 bp in length
*      91864 91963: gap of 100 bp
*      91964 104501: contig of 12538 bp in length
*      104502 104601: gap of 100 bp
*      104602 116857: contig of 12256 bp in length
*      116858 116957: gap of 100 bp
*      116958 127000: contig of 10043 bp in length
*      127001 127100: gap of 100 bp
*      127101 140329: contig of 13229 bp in length
*      140330 140429: gap of 100 bp
*      140430 154696: contig of 14267 bp in length.

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Location/Qualifiers

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1. 154696
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/db_xref="taxon:9606"
/clone="RP11-216h13"
/clone_id="RPC1-11 Human Male BAC"
1. 1088
/note="assembly_fragment"
1189. 2246
/note="assembly_fragment"
2347. 3505
/note="assembly_fragment"
3606. 4777
/note="assembly_fragment"
4878. 6634
/note="assembly_fragment"
6735. 8097
/note="assembly_fragment"
8198. 10306
/note="assembly_fragment"
10407. 12406
/note="assembly_fragment"
12507. 14219
/note="assembly_fragment"
14320. 16072
/note="assembly_fragment"
16173. 17723
/note="assembly_fragment"
17824. 19608
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19709. 22007
/note="assembly_fragment"
22108. 23950
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24051. 26881
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misc_feature      26982..29772
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misc_feature      29873..32307
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                  /note="assembly_fragment"
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                  /note="assembly_fragment"
misc_feature      42380..44940
                  /note="assembly_fragment"
                  clone_end:SP6
                  vector_side:left"
misc_feature      45041..48483
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                  /note="assembly_fragment"
                  clone_end:T7
                  vector_side:left"
misc_feature      52853..57771
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misc_feature      57872..61962
                  /note="assembly_fragment"

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Query Match 28.9%; Score 35; DB 2; Length 154696;
 Best Local Similarity 55.6%; Pred. No. 2.1;
 Matches 65; Conservative 1; Mismatches 51; Indels 0; Gaps 0;

```

QY 1 GCATTGGGCTTCCTCCTCAGAGCCCTCCGAGTGAGCTTCAGCTTTTCTCCTCATGGGG 60
    ||| || || |||| || |||| || || || || || || || || || || || || ||
DB 99631 GCAACTGCTGCTGAAGTCCTCCAGTCCTCCGCTGCGCTCCCTCCTCCTCCCTCC 99690
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QY 61 CAATCTYACTTTCGCTCAGTCTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCT 117
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DB 99691 CTCTCTATTCTCCTCCTCCTCCTCCCTCCCTCTTCTCCCTCCCGGCTGCTCT 99747
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Search completed: November 21, 2002, 03:10:02
 Job time : 3494 secs


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FT exon 2243..3940
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XX
XX WO200100803-A2.
XX 04-JAN-2001.
XX PD 21-JUN-2000; 2000WO-IB01011.
XX PF

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XX
XX 25-JUN-1999; 99US-0141032.
PR 20-DEC-1999; 99WO-IB02058.
PR 21-DEC-1999; 99US-0469099.
XX
XX (GEST ) GENSET.
XX
XX Yen F, Denison B, Bour B, Bihain B, Bougueleret L, Duclert A;
PI Dunas Milne Edwards J;
XX WPI; 2001-071485/08.
XX
XX Nucleic acids encoding apolipoprotein A-IV-related proteins (AA4RP) and
PT biallelic markers of AA4RP, useful for diagnosing lipid metabolism
PT related disorders and/or liver related disorders -
XX
XX Claim 3; Page 242-244; 260pp: English.
XX
XX The present sequence is that of an alternative genomic sequence
XX (see also AAF30035) of human apolipoprotein A-IV-related protein
XX (AA4RP). It encodes a 366-amino acid protein (see AAB20103). AA4RP
XX is differentially expressed in obese mouse models, indicating a role
XX in lipid metabolism related disorders. It appears to be the human
XX homologue of rat regeneration associated protein (RAP3), which is
XX believed to be involved in liver regeneration, and is likely to
XX have a similar function. It also shows 52% similarity to
XX apolipoprotein A-IV, and is likely to have a similar function. The
XX invention also provides AA4RP cDNAs (see AAF30036) and polypeptides,
XX biallelic markers identified in the AA4RP gene and from genomic
XX regions flanking the gene, and methods for genotyping a nucleic
XX acid containing 1 or more of the biallelic markers. Also provided
XX is a method for detecting a statistical correlation between a
XX biallelic marker allele and a phenotype and/or between a biallelic
XX marker haplotype and a phenotype. Diagnostic methods are provided
XX for determining whether an individual is at risk of developing a
XX lipid metabolism related disorder and/or a liver related disorder,
XX such as obesity, diabetes or coronary heart disease, and whether
XX the individual suffers from such a disorder as a result of a
XX polymorphism in the AA4RP gene. AA4RP DNA constructs can be
XX used to direct temporal and spatial AA4RP gene expression in
XX recombinant cell hosts and in transgenic animals. They can also
XX be used for recombinant production of AA4RP polypeptides, and as
XX probes and primers.
XX
XX Sequence 5381 BP; 1104 A; 1434 C; 1709 G; 1132 T; 2 other;
SQ
XX
XX Query Match 99.7%; Score 120.6; DB 22; Length 5381;
XX Best Local Similarity 100.0%; Pred. No. 8e-29;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 GCATTGGGCTTGCTCTCTCAGAGGCCCTCGAGTGGAGTTACGCTTTCTCATGGG 60
XX Db 252 GCATTGGGCTTGCTCTCTCAGAGGCCCTCGAGTGGAGTTACGCTTTCTCATGGG 311
XX Oy 61 CAAATCTYACTTTCGCTCAGTTCCTGCGGCGCAGTCCCTGGGCCAGATCCCTTTC 120
XX Db 312 CAAATCTYACTTTCGCTCAGTTCCTGCGGCGCAGTCCCTGGGCCAGATCCCTTTC 371
XX Oy 121 C 121
XX Db 372 C 372
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XX RESULT 2
XX AAF30035
XX ID AAF30035 standard; DNA; 81001 BP.
XX AC AAF30035;
XX XX
XX 23-APR-2001 (first entry)
XX DE Human apolipoprotein A-IV-related protein (AA4RP) gene.
XX

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FT misc_binding 77046..77070
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FT /note="20-853-415 probe"
XX
XX WO200100803-A2.
XX
XX 04-JAN-2001.
XX
XX 21-JUN-2000; 2000WO-1B01011.
XX
XX 25-JUN-1999; 99US-0141032.
XX 20-DEC-1999; 99WO-1B02058.
XX 21-DEC-1999; 99US-0469099.
XX
XX (GEST) GENSET.
XX
XX Yen F, Denison B, Bour B, Bihain B, Bougueleret L, Duclet A;
XX Dumas Mline Edwards J;
XX WPI: 2001-071485/08.
XX P-PSDB; AAB20103.
XX
XX Nucleic acids encoding apolipoprotein A-IV-related proteins (AA4RP) and
XX biallelic markers of AA4RP, useful for diagnosing lipid metabolism
XX related disorders and/or liver related disorders -
XX
XX Claim 1; Page 216-238; 260pp; English.
XX
XX The present sequence is that of the human apolipoprotein
XX A-IV-related protein (AA4RP) gene on chromosome 11. The gene
XX encodes a 366-amino acid protein (see AAB20103). AA4RP is
XX differentially expressed in obese mouse models, indicating a role
XX in lipid metabolism related disorders. It appears to be the human
XX homologue of rat regeneration associated protein (RAP3), which is
XX believed to be involved in liver regeneration, and is likely to
XX have a similar function. It also shows 52% similarity to
XX apolipoprotein A-IV, and is likely to have a similar function. The
XX invention also provides AA4RP cDNAs (see AAB20036) and polypeptides,
XX biallelic markers identified in the AA4RP gene and from genomic
XX regions flanking the gene, and methods for genotyping a nucleic
XX acid containing 1 or more of the biallelic markers. Also provided
XX is a method for detecting a statistical correlation between a
XX biallelic marker allele and a phenotype and/or between a biallelic
XX marker haplotype and a phenotype. Diagnostic methods are provided
XX for determining whether an individual is at risk of developing a
XX lipid metabolism related disorder and/or a liver related disorder,
XX
XX Query Match 99.7%; Score 120.6; DB 22; Length 81001;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-28;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 GCATTTGGCTTCTCTCTCAGAGCCCTTCGAGTGCAGCTTTTCTCATGCG 60
XX |||||||
XX DB 12280 GCATTTGGCTTCTCTCTCAGAGCCCTTCGAGTGCAGCTTTTCTCATGCG 12339
XX |||||||
XX QY 61 CAAATCTVACTTTCGCTCAGTTCCTGGGGCTAGAGTCCCTGGCCCAATGCTCTTGC 120
XX |||||||
XX DB 12340 CAAATCTVACTTTCGCTCAGTTCCTGGGGCTAGAGTCCCTGGCCCAATGCTCTTGC 12399
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XX QY 121 C 121
XX |
XX DB 12400 C 12400
XX
XX RESULT 3
XX ABR28380/c
XX ID ABR28380 standard; DNA; 5377 BP.
XX
XX ABR28380;
XX
XX 23-APR-2002 (first entry)
XX
XX DE DNA transcription associated complementary genomic DNA #127.

XX
XX DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
XX PNA; cytosine methylation state; SNP; retroviral infection; gene; ds;
XX single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
XX viral infection; Sezary syndrome; haematological disorder; tuberculosis;
XX immunological disorder; Werner syndrome; developmental disorder;
XX psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
XX neurodegenerative disorder; Maardenburg syndrome; Niemann-Pick disease;
XX myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
XX angiodysplasia; congenital heart disease; HDR syndrome; gene therapy;
XX polyglutamine disorder; solid tumour.
XX
XX Unidentified.
XX
XX WO200192565-A2.
XX
XX 06-DEC-2001.
XX
XX 06-APR-2001; 2001WO-EP03973.
XX
XX 06-APR-2000; 2000DE-1019058.
XX 07-APR-2000; 2000DE-1019173.
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI: 2002-090046/12.
XX
XX New nucleic acids or oligomers, useful for diagnosing or treating
XX diseases associated with DNA transcription, e.g. immunological
XX disorders, Werner syndrome, psoriasis, myocardial infarction, solid
XX tumours or cancer -
XX
XX Claim 1; SEQ ID No 254; 32pp; English.
XX
XX The invention relates to a nucleic acid, which comprises a segment of the
XX chemically pretreated DNA of genes associated with DNA transcription from
XX one of 346 sequences, and an oligomer, in particular an oligonucleotide
XX or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
XX to the chemically pretreated DNA of genes associated with DNA
XX transcription. The set of oligomer probes are useful for detecting the
XX cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
XX in a chemically pretreated genomic DNA. The nucleic acids are useful for
XX diagnosing or treating diseases associated with DNA transcription
XX (particularly with the methylation status), e.g. adenosine deaminase
XX deficiency, viral infection, retroviral infection, Werner syndrome,
XX haematological disorders, immunological disorders, Sezary syndrome,
XX tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,
XX neurological disorders, neurodegenerative disorders, Maardenburg
XX syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
XX infarction, hypertension, angiodysplasia, erythropoiesis, congenital heart
XX disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours
XX or cancer. Sequences ABR28127-ABR28472 represent DNA transcription
XX associated genomic DNA molecules of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from the
XX European Patent Office.
XX
XX Sequence 5377 BP; 1117 A; 176 C; 1481 G; 2603 T; 0 other:
XX
XX Query Match 44.1%; Score 53.4; DB 24; Length 5377;
XX Best Local Similarity 77.8%; Pred. No. 3.1e-07;
XX Matches 63; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
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XX DB 5376 TTCAGCTTTTCCATGAGGCAATCTVACTTTCGCTCAGTTCCTGGGGCTCAGAGTCC 5317
XX |||||
XX QY 101 CTGGCCCAATGCTCTTGC 121
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XX || ||||| || ||||| ||

DB 5316 CTAACCAATACCTCTACG 5296

RESULT 4

ID ABR28379 standard; DNA: 5377 BP.

ABR28379;

23-APR-2002 (first entry)

DNA transcription associated genomic DNA #127.

DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
 KM cytosine methylation state; SNP; retroviral infection; gene; ds;
 KM single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
 KM viral infection; Sezary syndrome; haematological disorder; tuberculosis;
 KM immunological disorder; Werner syndrome; developmental disorder;
 KM psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
 KM neurodegenerative disorder; Maendburg syndrome; Niemann-Pick disease;
 KM myelodysplastic syndrome; myocardial infarction; hyperlunism; arthritis;
 KM angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
 KM polyglutamine disorder; solid tumour.

Unidentified.

WO200192565-A2.

06-DEC-2001.

06-APR-2001: 2001WO-EP03973.

06-APR-2000: 2000DE-1019058.

07-APR-2000: 2000DE-1019173.

30-JUN-2000: 2000DE-1032529.

01-SEP-2000: 2000DE-1043826.

(EPIC-) EPICENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI: 2002-090046/12.

New nucleic acids or oligomers, useful for diagnosing or treating

diseases associated with DNA transcription, e.g. immunological

disorders, Werner syndrome, psoriasis, myocardial infarction, solid

tumours or cancer

Claim 1: SEQ ID No 253: 32pp: English.

The invention relates to a nucleic acid, which comprises a segment of the

chemically pretreated DNA of genes associated with DNA transcription from

one of 346 sequences, and an oligomer, in particular an oligonucleotide

or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical

to the chemically pretreated DNA of genes associated with DNA

transcription. The set of oligomer probes are useful for detecting the

cytosine methylation state and/or single nucleotide polymorphisms (SNPs)

in a chemically pretreated genomic DNA. The nucleic acids are useful for

diagnosing or treating diseases associated with DNA transcription

(particularly with the methylation status), e.g. adenosine deaminase

deficiency, viral infection, retroviral infection, Sezary syndrome,

Sequence 5377 BP: 1067 A: 176 C: 1712 G: 2422 T: 0 other:

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Best Local Similarity 68.8%; Pred. No. 0.0025;

Matches 55; Conservative 1; Mismatches 24; Indels 0; Gaps 0;

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1 GTTACGTTTTTTTATGCGGTAAATTTATTTTCCTTACGTTTGGCGTTACACTT 60

100 CCGGCCACATGCTCTG 119

61 TTTGGTTAGATGTTTTTG 80

RESULT 5

AAD26473/C

AAD26473 standard; cDNA: 2459 BP.

26-MAR-2002 (first entry)

Human kinase PKIN-26 cDNA.

Human; kinase; PKIN-26; cancer; leukaemia; adenocarcinoma; osteoporosis;
 KM immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
 KM Acquired immune deficiency Syndrome; AIDS; Addison's disease; anaemia;
 KM allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
 KM autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
 KM Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
 KM rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
 KM hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
 KM cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
 KM congestive heart failure; ischaemic heart disease; lung tumour; gout;
 KM fatty liver; Niemann-Pick's disease; gene therapy; ss.

Homo sapiens.

location/Qualifiers

key 107..2089

CD5 /tag-a

/product- "Human PKIN-26 protein"

WO200196547-A2.

20-DEC-2001.

14-JUN-2001: 2001WO-0519444.

15-JUN-2000: 2000US-212073P.

23-JUN-2000: 2000US-213467P.

30-JUN-2000: 2000US-215651P.

07-JUL-2000: 2000US-216605P.

13-JUL-2000: 2000US-218372P.

25-AUG-2000: 2000US-228056P.

(INCY-) INCYTE GENOMICS INC.

Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;

Gandhi AR, Tiriboulet CM, Walla NK, Yao MG, Lu DM, Greenwald SR,

Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;

Baughn MR, He A, Thornton M, Hafalla A, Patterson C, Gururajan R;

Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JJ, Ding L;

Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

WPI: 2002-090207/12.

P-PSDB: AAE16280.

New polypeptides, useful for diagnosing, treating or preventing

disorders of growth and development, cardiovascular and lipid, and

diseases such as cancer, comprise human kinase polypeptides

PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR P-PSDB: AAM39607.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 966; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 3446 BP; 759 A; 991 C; 1094 G; 602 T; 0 other:
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Query Match 24.3%; Score 29.4; DB 22; Length 3446;
Best Local Similarity 55.7%; Pred No 14;
Matches 54; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
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QY 7 GGGCTGCTCTCTCTCAGAGGCGCTGAGTGAGTTCAGCTTTTCTCATGGGCAATC 66
DB 2319 GTGCTACTGCTGCTCCCAAGGCGCTTCCAGACTTTTCCACGTTGCTGCTGCGACATG 2260
QY 67 TTAATTGCTGCTCCAGTCTCTGGGGCTCAGAGTCCCTG 103
DB 2259 ACACAAATCTCTCCGCTCCGAGGCGCAAGCTCCCG 2223
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ID AAK70514 standard; DNA; 12730 BP.
XX
AC AAK70514;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25326.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN HQ200157182-A2.
XX
PD 09-AUG-2001.

XX
PF 17-JAN-2001; 2001MO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-MAR-2000; 2000US-0198123.
PR 19-MAR-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.

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PR 29-SEP-2000: 2000US-0236369.
PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 02-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
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PR 20-OCT-2000: 2000US-0241808.
PR 20-OCT-2000: 2000US-0241809.
PR 20-OCT-2000: 2000US-0241826.
PR 01-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0246474.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
PR 08-NOV-2000: 2000US-0246477.
PR 08-NOV-2000: 2000US-0246478.
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PR 08-NOV-2000: 2000US-0246524.
PR 08-NOV-2000: 2000US-0246525.
PR 08-NOV-2000: 2000US-0246526.
PR 08-NOV-2000: 2000US-0246527.
PR 08-NOV-2000: 2000US-0246528.
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PR 08-NOV-2000: 2000US-0246611.
PR 08-NOV-2000: 2000US-0246613.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
PR 17-NOV-2000: 2000US-0249210.
PR 17-NOV-2000: 2000US-0249211.
PR 17-NOV-2000: 2000US-0249212.
PR 17-NOV-2000: 2000US-0249213.
PR 17-NOV-2000: 2000US-0249214.
PR 17-NOV-2000: 2000US-0249215.
PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249244.
PR 17-NOV-2000: 2000US-0249245.
PR 17-NOV-2000: 2000US-0249264.
PR 17-NOV-2000: 2000US-0249265.
PR 17-NOV-2000: 2000US-0249297.
PR 17-NOV-2000: 2000US-0249299.
PR 17-NOV-2000: 2000US-0249300.
PR 01-DEC-2000: 2000US-0250160.
PR 01-DEC-2000: 2000US-0250391.
PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
PR 06-DEC-2000: 2000US-0256719.
PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251989.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259676.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM,
XX
XX WPI: 2001-483426/52.
XX

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PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure: SEQ ID NO 25326; 3071bp + Sequence Listing: English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 12730 BP; 2891 A; 3333 C; 3652 G; 2854 T; 0 other:
Query Match 24.3%; Score 29.4; DB 22; Length 12730;
Best Local Similarity 55.7%; Pred. No. 20;
Matches 54; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
QY 7 GGGCTTGCTCTCCTCAGAGCCCTCGAGTGGAGTTCAGTTCCTCATGGGCAATC 66
DB 1999 GTGCTTACCTGCTGCTCCCAAGGCCCTTCACACTTTTTCACCTGCTGCTGCACATG 1940
QY 67 TVACTTTGCTCGAGTTCCTCGGCGCTCAGAGTCCCG 103
DB 1939 ACACAATCTCTCCGCTCCCTCGAGGCCAGCTCCCG 1903
RESULT 9
AAK99032
ID AAK99032 standard; cDNA; 845 BP.
XX
XX AAK99032;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX Human validated cancer cell derived cDNA #354.
DE
XX
XX Cancer: human; colon; breast; lung; transmembrane receptor; ATPase;
XX integral membrane protein; aspartyl protease; GATA family; wnt family;
XX transcription factor; G-protein alpha subunit; protein phosphatase;
XX phospholipase; protein kinase; diacylglycerol binding protein; tyrosin;
XX protein kinase; tyrosine phosphatase; developmental signalling protein;
XX WW/rsp/WWP domain; therapy; forensic; genetic mapping; diagnostic;
XX detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
XX Wilms' tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
XX leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
XX prostate; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9933982-A2.
PN
XX
XX 08-JUL-1999.
PD
XX
XX 22-DEC-1998; 98WO-US27610.
PF
XX
XX 21-DEC-1998; 98US-0217471.
XX 23-DEC-1997; 97US-0068755.
PR 03-APR-1998; 98US-0080664.
PR 21-OCT-1998; 98US-0105234.
PR 27-OCT-1998; 98US-0105877.

```


[illegible]

XX	(HUMA-)	HUMAN GENOME SCI INC.
PA		
XX	Rosen CA,	Barash SC, Ruben SM;
PI		
XX	WPI; 2001-465570/50.	
DR		
XX		
PT	Isolated nucleic acid molecule encoding a reproductive system antigen	
PR	is used in preventing, treating or ameliorating a medical condition	
XX		
PS	Disclosure: SEQ ID NO 7666; 1297bp + Sequence Listing: English.	
CC	The present invention provides the protein and coding sequences of a	
CC	number of human reproductive system related antigens. These can be used	
CC	in the prevention and treatment of reproductive system disorders,	
CC	including cancer. The present sequence is a genomic sequence encoding a	
CC	protein of the invention.	
XX		
SQ	Sequence 1768 BP; 445 A; 440 C; 461 G; 422 T; 0 other;	
Query Match	23.8%; Score 28.8; DB 22; Length 1768;	
Best Local Similarity	55.1%; Pred. No. 18;	
Matches	54; Conservative 1; Mismatches 43; Indels 0; Gaps 0;	
OY	12 TCCTTCCTCAGACAGCCCTCGCGATGCACTTTCCTCATGGGCAAAATCYACT 71	
DB	1100 TCGTATTGTGCAAATGTGCTGAAGAAGACAGTAGTGCTCTTACCCTTAGAGAGAGGCTCCT 1159	
OY	72 TTGGCTCCAGTTCTCTGGGGCTTCAGAGTCCCTGCTGCCACG 109	
DB	1160 TACACTGACATTCAAAGTCTCAATGACCCGCCCCACG 1197	
RESULT 11		
AAL04979		
ID	AAL04979 standard; DNA; 1768 BP.	
XX		
XX	AAL04979;	
DT		
XX	21-NOV-2001 (first entry)	
DE		
XX	Human reproductive system related antigen DNA SEQ ID NO: 7667.	
XX	Human; reproductive system related antigen; reproductive system disorder;	
KM	cancer; gene therapy; ds.	
XX		
OS	Homo sapiens.	
PN		
XX	WO200155320-A2.	
PD		
XX	02-AUG-2001.	
PF		
XX	17-JAN-2001; 2001WO-US01339.	
XX		
PR	31-JAN-2000; 2000US-0179065.	
PR	04-FEB-2000; 2000US-0180628.	
PR	24-FEB-2000; 2000US-0184664.	
PR	02-MAR-2000; 2000US-0186350.	
PR	16-MAR-2000; 2000US-0189874.	
PR	17-MAR-2000; 2000US-0190076.	
PR	18-APR-2000; 2000US-0198123.	
PR	19-MAY-2000; 2000US-0205515.	
PR	07-JUN-2000; 2000US-0209467.	
PR	28-JUN-2000; 2000US-0214886.	
PR	30-JUN-2000; 2000US-0215135.	
PR	07-JUL-2000; 2000US-0216647.	
PR	11-JUL-2000; 2000US-0217487.	
PR	11-JUL-2000; 2000US-0217496.	
PR	14-JUL-2000; 2000US-0218299.	
PR	26-JUL-2000; 2000US-0220963.	
PR	26-JUL-2000; 2000US-0220964.	
PR	14-AUG-2000; 2000US-0224518.	

DB 1160 TACACTGACATTCAAGTCTCATGACCCGCCGAG 1197

RESULT 12

ABL97871
ID ABL97871 standard; DNA; 1768 BP.

XX ABL97871;

AC 21-JUN-2002 (first entry)

XX Human testicular antigen encoding DNA fragment SEQ ID NO: 2523.

XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;

XX reproductive system disorder; urinary system disorder; gene therapy;

XX cardiovascular disorder; respiratory disorder; neurological disorder;

XX gastrointestinal disease; infection; cytostatic; gene; ds.

XX Homo sapiens.

XX WO20015317-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01329.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

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PR 14-SEP-2000; 2000US-0232401.

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PR 14-SEP-2000; 2000US-0233065.

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PR 21-SEP-2000; 2000US-0234274.

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PR 27-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.

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PR 29-SEP-2000; 2000US-0236369.

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PR 02-OCT-2000; 2000US-0237037.

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PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.

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PR 13-OCT-2000; 2000US-0239937.

PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241221.

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PR 20-OCT-2000; 2000US-0241786.

PR 20-OCT-2000; 2000US-0241787.

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PR 01-NOV-2000; 2000US-0244617.

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PR 08-NOV-2000; 2000US-0246525.

PR 08-NOV-2000; 2000US-0246526.

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PR 08-NOV-2000; 2000US-0246610.

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PR 08-NOV-2000; 2000US-0246613.

PR 17-NOV-2000; 2000US-0249207.

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PR 01-DEC-2000; 2000US-0250391.
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PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides,
XX useful for preventing, diagnosing and/or treating testicular cancer -
XX
XX
XX Disclosure; SEQ ID NO 2523; 766pp; English.
XX
XX
XX The present invention provides the protein and coding sequences of 973
XX human testicular antigens, and fragments of their genomic sequences. The
XX sequences can be used in the treatment of cardiovascular, urinary system,
XX reproductive system, immune, respiratory, neurological and
XX gastrointestinal disorders, infections, and particularly cancer,
XX especially testicular cancers. The present sequence is a DNA encoding a
XX protein fragment of the invention.
XX
XX Sequence 1768 BP; 445 A; 440 C; 461 G; 422 T; 0 other;
XX
XX
XX Query Match 23.8%; Score 28.8; DB 23; Length 1768;
XX Best Local Similarity 55.1%; Pred. No. 18;
XX Matches 54; Conservative 1; Mismatches 43; Indels 0; Gaps 0;
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XX 12 TGCCTCCAGAGGCCGCCGAGTTCAGTTCCTTCATGCGCAATCTYACT 71
XX 1100 TGTATATGCAATGTGCTGAAGACAGATGTCCTTACCTTAGAGAGAGGCTCT 1159
XX
XX 72 TTGCTCCAGTTCTCTGGGCTCAGAGTCCCTGCGCCAG 109
XX 1160 TACACTGACATTCATCAAGTCTCAATGACCCGCCCCAG 1197
XX
XX
XX RESULT 13
XX ABL97872
XX ID ABL97872 standard; DNA; 1768 BP.
XX
XX ABL97872;
XX
XX 21-JUN-2002 (first entry)
XX
XX Human testicular antigen encoding DNA fragment SEQ ID NO: 2524.
XX
XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;
XX reproductive system disorder; urinary system disorder; gene therapy;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disease; infection; cytostatic; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200155317-A2.
XX
XX 02-AUG-2001.
XX
XX

PF 17-JAN-2001; 2001WO-US01329.
XX
XX 31-JAN-2000; 2000US-0179065.
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XX 02-MAR-2000; 2000US-0186350.
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PR 08-DEC-2000; 2000US-0251989.
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PR 11-DEC-2000; 2000US-0256097.
PR 05-JAN-2001; 2001US-0253978.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides,

PT useful for preventing, diagnosing and/or treating testicular cancer
XX
XX Disclosure; SEQ ID NO 2524; 766pp; English.
PS
XX The present invention provides the protein and coding sequences of 973
XX human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a DNA encoding a
CC protein fragment of the invention.
XX
SQ Sequence 1768 BP; 445 A; 441 C; 459 G; 422 T; 1 other;
Query Match 23.8%; Score 28.8; DB 23; Length 1768;
Best Local Similarity 35.18; Pred. No. 18;
Matches 54; Conservative 1; Mismatches 43; Indels 0; Gaps 0;
OY 12 TGCCTCCTCAGAGCGCCCTGCGAGTGAGTTCAGCTTTTCTCATGAGGCAATCTACT 71
DB 1100 TGCCTCCTCAGAGCGCCCTGCGAGTGAGTTCAGCTTTTCTCATGAGGCAATCTACT 1159
OY 72 TTGCTCCAGTTCCTGCGAGTTCAGAGTCCCTGCCCCAG 109
DB 1160 TACACTGACATTCAGAAAGTCTCATGAGTCCGCCCCAG 1197
RESULF 14
ABNS59848
ID ABNS59848 standard; cDNA; 3549 BP.
XX
XX ABNS59848;
AC
XX
XX 28-JUN-2002 (first entry)
DT
XX
XX Novel human coding sequence SEQ ID NO: 259.
DE
XX
XX Human; antihaemic; vulnery; antiinflammatory; immunomodulator;
KM antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KM neuroprotective; antiparkinsonian; protein therapy; EST;
KM expressed sequence tag; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200222660-A2.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US26015.
PF
XX
XX 11-SEP-2000; 2000US-0659671.
PR
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
PI WPI; 2002-292408/33.
DR
XX
XX P-PSDB; ABB97435.
DR
XX
XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
XX Clatm 1; SEQ ID NO 259; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activity or inhibit e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions


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/tissue_type="iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from

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/db_xref="taxon:9606"
/clone_lib="CN0155"
/dev_stage="Adult"
/notes="Organ: colon-normal; Vector: puc18; Site_1: Smar; Site_2: Smar; A mini-library was made by cloning products

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```

LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3/regulatory region
NAME/KEY: allele
LOCATION: 319
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 3213
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: conflict
LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
NAME/KEY: primer_bind
LOCATION: 1..11022
OTHER INFORMATION: 17-42..rp
NAME/KEY: primer_bind
LOCATION: 553..11575
OTHER INFORMATION: 17-42..rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39..pu
NAME/KEY: primer_bind
LOCATION: 1246..12267
OTHER INFORMATION: 17-40..pu
NAME/KEY: primer_bind
LOCATION: 1441..12461
OTHER INFORMATION: 17-39..rp complement
NAME/KEY: primer_bind
LOCATION: 1632..12651
OTHER INFORMATION: 17-40..rp complement
NAME/KEY: primer_bind
LOCATION: 2964..13984
OTHER INFORMATION: 17-41..pu
NAME/KEY: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41..rp complement
NAME/KEY: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 320..338
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 3194..3212
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 3214..3232
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: misc_binding
LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 3201..3225
OTHER INFORMATION: 17-41-250.probe
US-09-750-580-4

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Query Match          99.7%: Score 120.6; DB 4; Length 5381;
Best Local Similarity 100.0%: Pred. No. 2e-30;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 GCATTTGGCTGCTCTCCAGAGCCCTGCAGTGCAGTTCCATGAGG 60
DB      252 GCATTTGGCTGCTCTCCAGAGCCCTGCAGTGCAGTTCCATGAGG 311
OY      61 CAAATCTACTTTCGTCAGTTCCTGGGGCTCAGAGTCCCGCCCAATGCTTTCG 120
DB      312 CAAATCTACTTTCGTCAGTTCCTGGGGCTCAGAGTCCCGCCCAATGCTTTCG 371

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OY      121 C 121
DB      372 C 372

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RESULT 2
US-09-750-580-1
Sequence 1, Application US/09750580
Patent No. 645280
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebdets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US2 CIP
CURRENT APPLICATION NUMBER: US/09/750,580
PRIORITY FILING DATE: 2000-12-28
PRIORITY APPLICATION NUMBER: US 09/599,362
PRIORITY FILING DATE: 2000-06-21
PRIORITY APPLICATION NUMBER: PCT/IB00/0101
PRIORITY FILING DATE: 2000-06-21
PRIORITY APPLICATION NUMBER: PCT/IB99/02058
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: US 49/469/099
PRIORITY FILING DATE: 1999-12-21
PRIORITY APPLICATION NUMBER: US 60/113,686
PRIORITY FILING DATE: 1998-12-22
PRIORITY APPLICATION NUMBER: US 60/141,032
PRIORITY FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5/regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 15969..17969
OTHER INFORMATION: 3/regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele

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LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.fp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 77039..77057

OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_bind
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_bind
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_bind
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_bind
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_bind
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_bind
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 99.7%; Score 120.6; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred. No. 4; 7e-30;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTTGGGCTGCTCTCTCGAGGCGCTGGAGTGAATTCAGTTTCTCATGGGG 60
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DB 12280 GCATTTGGGCTGCTCTCTCGAGGCGCTGGAGTGAATTCAGTTTCTCATGGGG 12339
QY 61 CAATCTVACTTTCGCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTTTCG 120
|||||
DB 12340 CAATCTVACTTTCGCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTTTCG 12399

QY 121 C 121
DB 12400 C 12400

RESULT 3
US-09-245-041-5/c
; Sequence 5, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 90050
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-245-041-5

Query Match 22.3%; Score 27; DB 4; Length 90050;
Best Local Similarity 57.8%; Pred. No. 25;
Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 21 CAGAGCCCTCGAGTGGAGTTCAGTTTCTCATGGGCAATCTVACTTTCGCTCA 80
|||||
DB 33058 CAGAGCCCTCGAGTGGAGTTCAGTTTCTCATGGGCAATCTVACTTTCGCTCA 32999

QY 81 GTCTGCGGCTCAGAGTCCCTG 103
 32998 GTCCACAGGATCTGATCCAG 32976

RESULT 4

US-09-342-681C-8/C
 : Sequence 8, Application US/09342681C
 : Patent No. 6355782
 : GENERAL INFORMATION:
 : APPLICANT: Zonana et al.
 : TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
 : FILE REFERENCE: 52978
 : CURRENT APPLICATION NUMBER: US/09/342,681C
 : PRIOR FILING DATE: 1999-06-29
 : PRIOR APPLICATION NUMBER: 60/092,279
 : PRIOR FILING DATE: 1998-07-09
 : PRIOR APPLICATION NUMBER: 60/112,366
 : NUMBER OF SEQ ID NOS: 123
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 8
 : LENGTH: 977
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-342-681C-8

Query Match 22.1%; Score 26.8; DB 4; Length 977;
 Best Local Similarity 55.7%; Pred. No. 6.8;

Matches 49; Conservative 1; Mismatches 38; Indels 0; Gaps 0;

QY 10 CTGCTCTCTCAGAGCCCTGCGAGTGAGTTCAGCTTTCTCATGGGCAAACTYA 69
 524 CCTTTCCTCCCTCAGAGCGAGTGCTGTGAGCCATGCTCCCTGACGCGCTG 465
 QY 70 CTGCTCAGAGTCTCGGGGCTCAGAG 97
 464 TGTAGCTTTATTTCTCCAGGCTCAGAG 437

RESULT 5

US-09-097-319A-19/C
 : Sequence 19, Application US/09097319A
 : Patent No. 6384207
 : GENERAL INFORMATION:
 : APPLICANT: Ainley, Michael
 : APPLICANT: Armstrong, Katherine
 : APPLICANT: Belmar, Scott
 : APPLICANT: Folkerts, Otto
 : APPLICANT: Hopkins, Nicole
 : APPLICANT: Menke, Michael A.
 : APPLICANT: Petolino, Joseph P.
 : APPLICANT: Paredy, Dayakar
 : APPLICANT: Smith, Kelley
 : APPLICANT: Woosley, Aaron
 : TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
 : NUMBER OF SEQUENCES: 59
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dowelanco Patent Department
 : STREET: 9330 Zionsville Road
 : CITY: Indianapolis
 : STATE: Indiana
 : COUNTRY: USA
 : ZIP: 46268
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/097,319A
 : FILING DATE:
 : CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Stuart, Donald R.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317 337 4816
 TELEFAX: 317 337 4847
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9335 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA
 US-09-097-319A-19

Query Match 22.1%; Score 26.8; DB 4; Length 9335;
 Best Local Similarity 52.7%; Pred. No. 14;

Matches 58; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 8 GAGCTGCTCTCTCAGAGCCCTGCGAGTGAGTTCAGCTTTCTCATGGGCAAACT 67
 5920 GCGATGTCGCGCTCGGTGCGACGCGGATGTCGCGCGCGCTTCTGCGGCGCATGCT 5861
 QY 68 YACTTCGCTCAGAGTTCGCGGCTCAGAGTTCCTGCGCGCGCATGCTCT 117
 5860 GAATGCTTATCCGCTGCTGGAACAAATGCGCCAGATCCGCTCGAGCT 5811

RESULT 6

US-09-173-300-52/C
 : Sequence 52, Application US/09173300
 : Patent No. 6451581
 : GENERAL INFORMATION:
 : APPLICANT: Falco, Saverio Carl
 : APPLICANT: Hiltz, William D.
 : APPLICANT: Kinney, Anthony J.
 : APPLICANT: Cahoon, Rebecca E.
 : APPLICANT: Rafalski, J. Antoni
 : TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
 : FILE REFERENCE: BB-1126
 : CURRENT APPLICATION NUMBER: US/09/173,300
 : CURRENT FILING DATE: 1998-10-15
 : EARLIER APPLICATION NUMBER: 60/063,423
 : EARLIER FILING DATE: 1997 October 28
 : NUMBER OF SEQ ID NOS: 54
 : SOFTWARE: Microsoft Word Version 7.0A
 : SEQ ID NO 52
 : LENGTH: 995
 : TYPE: DNA
 : ORGANISM: Trifolium aestivum
 : US-09-173-300-52

Query Match 22.0%; Score 26.6; DB 4; Length 995;
 Best Local Similarity 64.4%; Pred. No. 8;

Matches 38; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

QY 10 CTGCTCTCTCAGAGCCCTGCGAGTGAGTTCAGCTTTCTCATGGGCAAACTYA 68
 778 CTTCATCTCCGACAGAGCTCGGCTGCTAAGCTGATCTTTCCCTCATGACGACCTTTC 720

RESULT 7

US-08-583-562B-9
 : Sequence 9, Application US/08583562B
 : Patent No. 5922570
 : GENERAL INFORMATION:
 : APPLICANT: Staunton, Donald
 : APPLICANT: Harris, Edith
 : TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
 : NUMBER OF SEQUENCES: 36
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 : STREET: 233 South Wacker Drive, 6300 Sears Tower

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-6300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1125
US-08-583-562B-9

Query Match 21.8%; Score 26.4; DB 2; Length 1125;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGCGAGTTCAGCTTTCTCATGAGGCAATCTYACTTGCCT 77
DB 354 CCCCTGCGCGGTGTGACTGAGCGAGATTGTGCCATGCGAAGACTCACACTGCCT 413

QY 78 CCACTTCCTG 87
DB 414 CCGGTTGTG 423

RESULT 8
US-08-779-113-9
Sequence 9, Application US/08779113
Patent No. 5948891
GENERAL INFORMATION:
APPLICANT: Staunton, Donald E.
APPLICANT: Harris, Edith S.
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,113
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greta E. No. 5948891and

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1125
US-08-779-113-9

Query Match 21.8%; Score 26.4; DB 2; Length 1125;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGCGAGTTCAGCTTTCTCATGAGGCAATCTYACTTGCCT 77
DB 354 CCCCTGCGCGGTGTGACTGAGCGAGATTGTGCCATGCGAAGACTCACACTGCCT 413

QY 78 CCACTTCCTG 87
DB 414 CCGGTTGTG 423

RESULT 9
US-08-583-562B-11
Sequence 11, Application US/08583562B
Patent No. 5922570
GENERAL INFORMATION:
APPLICANT: Staunton, Donald
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-6300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1449

US-08-583-562B-11

Query Match 21.8%; Score 26.4; DB 2; Length 1494;

Best Local Similarity 60.0%; Pred. No. 11;

Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGGAGTTCACCTTTCCATGCGCAAAATCTYACTTCCGT 77

DB 48 CCCCTCTGCGCTGTGACTGAGGACAGATTTGCCCCATGGGAGAACTCAGACTGCGT 107

QY 78 CCAATTCTCG 87

DB 108 CCGGTTTGTG 117

RESULT 10

US-08-779-113-11

; Sequence 11, Application US/08779113

; Patent No. 5948891

; GENERAL INFORMATION:

; APPLICANT: Staunton, Donald E.

; TITLE OF INVENTION: Cytoplasmic Modulators of Integrin

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 233 South Wacker Drive, 6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,113

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Greta E. No. 5948891and

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/33773

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1494 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1449

; US-08-779-113-11

Query Match 21.8%; Score 26.4; DB 2; Length 1494;

Best Local Similarity 60.0%; Pred. No. 11;

Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGGAGTTCACCTTTCCATGCGCAAAATCTYACTTCCGT 77

DB 48 CCCCTCTGCGCTGTGACTGAGGACAGATTTGCCCCATGGGAGAACTCAGACTGCGT 107

QY 78 CCAATTCTCG 87

DB 108 CCGGTTTGTG 117

RESULT 11

US-08-583-562B-1

; Sequence 1, Application US/08583562B

; Patent No. 5922570

; GENERAL INFORMATION:

; APPLICANT: Staunton, Donald

; TITLE OF INVENTION: Cytoplasmic Modulators of Integrin

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 233 South Wacker Drive, 6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,562B

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Williams Jr., Joseph A.

; REGISTRATION NUMBER: 38,659

; REFERENCE/DOCKET NUMBER: 27866/33033

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2574 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..2574

; US-08-583-562B-1

Query Match 21.8%; Score 26.4; DB 2; Length 2574;

Best Local Similarity 60.0%; Pred. No. 13;

Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGGAGTTCACCTTTCCATGCGCAAAATCTYACTTCCGT 77

DB 1170 CCCCTCTGCGCTGTGACTGAGGACAGATTTGCCCCATGGGAGAACTCAGACTGCGT 1229

QY 78 CCAATTCTCG 87

DB 1230 CCGGTTTGTG 1239

RESULT 12

US-08-779-113-1

; Sequence 1, Application US/08779113

; Patent No. 5948891

; GENERAL INFORMATION:

; APPLICANT: Staunton, Donald E.

; TITLE OF INVENTION: Cytoplasmic Modulators of Integrin

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 233 South Wacker Drive, 6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,113
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greta E. No. 5948891and
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2574 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2574
US-08-779-113-1

Query Match 21.8%; Score 26.4; DB 2; Length 2574;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGGAGAGGAGTTCAGCTTTCATGCGGCAATCTVACTTTCGCT 77
DB 1170 CCCCTCTGGCCCTGTACTGAGGACAGATGTGCCATGGGGAAGACTCACACTGCCG 1229

QY 78 CCAAGTTCCTG 87
DB 1230 CCGGTTTGTG 1239

RESULT 13
US-08-724-394A-20
Sequence 20, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A. 35,136
REGISTRATION NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..246240
OTHER INFORMATION: /note="HLA-H.CONFIG"
US-08-724-394A-20

Query Match 21.8%; Score 26.4; DB 2; Length 246240;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 37 GCAATTCACTTTCTCCATGCGGCAATCTVACTTTCCTCCAGTTCCTGGGCTCAGA 96
DB 160999 GCGCTTCGCCCTATTCTTCTTGCGCGCCGCTTCTAGGCTTGACACCTGGGCTTGGC 161058

QY 97 GTCCCTGGCC 106
DB 161059 GCGCTTGGCC 161068

RESULT 14
US-08-724-394A-21
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Krommal, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 02:06:48 ; Search time 82 Seconds
(without alignments)
558,858 Million cell updates/sec

Title: US-09-842-364-1_COPY_12280_12400

Perfect score: 121
Sequence: 1 gcaattggctgctctctc.....tggccagatgcctctgctc 121

Scoring table: IDENTITY NDC
Gapop 10.0, Gapext 1.0

Searched: 335578 seqs, 18936513 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications NA*

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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120.6	99.7	5381	10 US-09-751-877-4	Sequence 4, Appl1
2	120.6	99.7	81001	10 US-09-751-877-1	Sequence 1, Appl1
3	30.8	25.5	317	10 US-09-728-446-405	Sequence 405, Appl
4	27.8	23.0	504	10 US-09-783-590-5953	Sequence 5953, Ap
5	27.8	23.0	1026	10 US-09-886-055-28	Sequence 28, Appl1
6	27.8	23.0	1091	9 US-10-011-597-1	Sequence 1, Appl1
7	27.8	23.0	3000	10 US-09-919-172-13	Sequence 13, Appl1
8	27.2	22.5	222	10 US-09-783-590-11626	Sequence 11626, A
9	27.2	22.3	524	10 US-09-864-761-15294	Sequence 15294, A
10	27.2	22.3	4926	10 US-09-728-952-18	Sequence 18, Appl1
11	27.2	22.3	90050	10 US-09-893-238-5	Sequence 5, Appl1
12	26.8	22.1	1147	10 US-09-789-561-57	Sequence 57, Appl1
13	26.8	22.1	15980	10 US-09-764-864-1714	Sequence 1714, Ap
14	26.6	22.0	472	10 US-09-864-761-5516	Sequence 5516, Ap
15	26.6	22.0	494	10 US-09-917-800A-61	Sequence 61, Appl
16	26.6	22.0	995	12 US-10-027-450-53	Sequence 52, Appl
17	26.4	21.8	341	10 US-09-764-869-538	Sequence 538, Appl
18	26.4	21.8	389	10 US-09-864-761-25624	Sequence 25624, A
19	26.4	21.8	522	10 US-09-864-761-8963	Sequence 8963, Ap

C 20	26.4	21.8	1391	10 US-09-969-708-480	Sequence 480, App
C 21	26.4	21.8	1391	10 US-09-880-107-3740	Sequence 3740, Ap
C 22	26.4	21.8	5607	9 US-10-109-605-92	Sequence 92, Appl
C 23	26.4	21.5	1138	10 US-09-778-844-165	Sequence 165, Appl
C 24	26.4	21.5	1137	10 US-09-778-844-164	Sequence 164, App
C 25	26.4	21.5	1137	10 US-09-778-844-166	Sequence 166, App
C 26	26.4	21.5	1206	12 US-10-062-254-143	Sequence 143, App
C 27	26.4	21.5	1416	12 US-10-062-254-145	Sequence 145, App
C 28	25.6	21.2	470	10 US-09-864-761-15312	Sequence 15312, A
C 29	25.6	21.2	3741	10 US-09-803-286A-1	Sequence 1, Appl1
C 30	25.6	21.0	4744	10 US-09-880-107-3459	Sequence 3459, Ap
C 31	25.2	20.8	350	10 US-09-878-574-3008	Sequence 3008, Ap
C 32	25.2	20.8	424	10 US-09-867-550-705	Sequence 705, App
C 33	25.2	20.8	674	10 US-09-764-878-47	Sequence 47, Appl
C 34	25.2	20.8	674	10 US-09-764-860-184	Sequence 184, App
C 35	25.2	20.8	5265	10 US-09-920-300A-1663	Sequence 1663, Ap
C 36	25.2	20.8	5265	12 US-10-033-528-1663	Sequence 1663, Ap
C 37	25.2	20.8	5629	10 US-09-969-347-208	Sequence 208, App
C 38	25.2	20.8	5760	12 US-10-044-090-67	Sequence 67, Appl
C 39	25.2	20.8	5762	10 US-09-919-172-55	Sequence 55, Appl
C 40	25.2	20.7	720	10 US-09-815-242-9471	Sequence 9471, Ap
C 41	25.2	20.7	720	10 US-09-815-242-9471	Sequence 9471, Ap
C 42	24.8	20.5	261	9 US-09-728-444-1027	Sequence 1027, Ap
C 43	24.8	20.5	1632	10 US-09-887-381-3	Sequence 3, Appl1
C 44	24.8	20.5	1827	10 US-09-974-298-174	Sequence 174, App
C 45	24.8	20.5	1827	10 US-09-919-172-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-751-877-4
; Sequence 4, Application US/09751877
; Patent No. US20020142949A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Dumais, Milne Edwards, Jean-Baptiste
; APPLICANT: Duclet, Aymeric
; APPLICANT: Bouget, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US3.PG
; CURRENT APPLICATION NUMBER: US/09/751,877
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 4
; LENGTH: 5381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..918
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 919..930
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 1442..1498
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 1613..1724
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 2243..3940
; OTHER INFORMATION: exon 4
; NAME/KEY: misc.feature
; LOCATION: 3941..5381

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OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 319
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 323
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: conflict
LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
NAME/KEY: primer_bind
LOCATION: 1..11022
OTHER INFORMATION: 17-42-.pu
NAME/KEY: primer_bind
LOCATION: 553..11575
OTHER INFORMATION: 17-42-.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39-.pu
NAME/KEY: primer_bind
LOCATION: 1246..12287
OTHER INFORMATION: 17-40-.pu
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LOCATION: 1441..12461
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LOCATION: 2964..13984
OTHER INFORMATION: 17-41-.pu
NAME/KEY: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41-.rp complement
NAME/KEY: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 320..338
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
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OTHER INFORMATION: 17-41-250.mis
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LOCATION: 3214..3232
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: misc_binding
LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
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US-09-751-877-4

Query Match          99.7%; Score 120.6; DB 10; Length 5381;
Best Local Similarity 100.0%; Pred. No. 9.3e-31;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-751-877-1
Sequence 1. Application US/09751877
Patent No. US20020142949A1
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouguetel, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89,US3,REG
CURRENT APPLICATION NUMBER: US/09/751,877
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
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OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
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LOCATION: 929..949
OTHER INFORMATION: 20-828-.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
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NAME/KEY: primer_bind
LOCATION: 12581..12603
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LOCATION: 15460..15482
OTHER INFORMATION: 17-41-TP complement
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LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841-TP complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
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NAME/KEY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
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OTHER INFORMATION: 20-853-TP complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
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LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
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LOCATION: 12328..12346
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LOCATION: 12348..12356
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LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
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OTHER INFORMATION: 17-41-250.mis complement
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LOCATION: 45423..45441
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NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
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OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
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OTHER INFORMATION: 20-841-149.probe

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NAME/KEY: misc_binding
LOCATION: 45430..45454
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LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-751-877-1

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Query Match 99.7% Score 120.6; DB 10; Length 81001;
 Best Local Similarity 100.0%; Pred. No. 2; 3e-30;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12340 CAAATCTACTTTCGCTCCAGTTCCTGAGGCTCAGATCCCTGAGATGCTTTC 12399
QY 121 C 121
DB 12400 C 12400

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RESULT 3
US-09-728-446-405
Sequence 405, Application US/09728446
Patent No. US20020081668A1
GENERAL INFORMATION:
APPLICANT: Friedlich, Glenn
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020081668A1 Murine Polynucleotide Sequences
FILE REFERENCE: IEX-0101-USA
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,270
PRIORITY FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1461
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 405
LENGTH: 317
TYPE: DNA
ORGANISM: Mus musculus
US-09-728-446-405

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Query Match 25.5% Score 30.8; DB 10; Length 317;
 Best Local Similarity 58.9%; Pred. No. 0.25;
 Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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DB 167 TCAGAGGCCCTCGAGTTCCTTCATGAGCAATCTTTCGCTCC 226
QY 80 AGTTCCTGGGCTCAGAGTCCCTGAGCCAG 109
DB 227 AGTTCAGAGGAATGACACCTTGAGAG 256

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RESULT 4
US-09-783-590-5953
Sequence 5953, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16-2C1

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1	CURRENT APPLICATION NUMBER: US/09/783,593
2	CURRENT FILING DATE: 2000-02-15
3	PRIOR APPLICATION NUMBER: 08/420,856
4	PRIOR FILING DATE: 1995-04-12
5	PRIOR APPLICATION NUMBER: 08/346,731
6	PRIOR FILING DATE: 1994-11-21
7	NUMBER OF SEQ ID NOS: 12485
8	SOFTWARE: PatentIn Ver. 2.0
9	SEQ ID NO 5953
10	LENGTH: 504
11	TYPE: DNA
12	ORGANISM: Homo sapiens
13	FEATURE:
14	NAME/KEY: misc feature
15	LOCATION: (61)
16	OTHER INFORMATION: n equals a,t,g, or c
17	NAME/KEY: misc feature
18	LOCATION: (62)
19	OTHER INFORMATION: n equals a,t,g, or c
20	NAME/KEY: misc feature
21	LOCATION: (78)
22	OTHER INFORMATION: n equals a,t,g, or c
23	NAME/KEY: misc feature
24	LOCATION: (96)
25	OTHER INFORMATION: n equals a,t,g, or c
26	NAME/KEY: misc feature
27	LOCATION: (115)
28	OTHER INFORMATION: n equals a,t,g, or c
29	NAME/KEY: misc feature
30	LOCATION: (116)
31	OTHER INFORMATION: n equals a,t,g, or c
32	NAME/KEY: misc feature
33	LOCATION: (125)
34	OTHER INFORMATION: n equals a,t,g, or c
35	NAME/KEY: misc feature
36	LOCATION: (126)
37	OTHER INFORMATION: n equals a,t,g, or c
38	NAME/KEY: misc feature
39	LOCATION: (127)
40	OTHER INFORMATION: n equals a,t,g, or c
41	NAME/KEY: misc feature
42	LOCATION: (130)
43	OTHER INFORMATION: n equals a,t,g, or c
44	NAME/KEY: misc feature
45	LOCATION: (132)
46	OTHER INFORMATION: n equals a,t,g, or c
47	NAME/KEY: misc feature
48	LOCATION: (146)
49	OTHER INFORMATION: n equals a,t,g, or c
50	NAME/KEY: misc feature
51	LOCATION: (150)
52	OTHER INFORMATION: n equals a,t,g, or c
53	NAME/KEY: misc feature
54	LOCATION: (153)
55	OTHER INFORMATION: n equals a,t,g, or c
56	NAME/KEY: misc feature
57	LOCATION: (164)
58	OTHER INFORMATION: n equals a,t,g, or c
59	NAME/KEY: misc feature
60	LOCATION: (170)
61	OTHER INFORMATION: n equals a,t,g, or c
62	NAME/KEY: misc feature
63	LOCATION: (188)
64	OTHER INFORMATION: n equals a,t,g, or c
65	NAME/KEY: misc feature
66	LOCATION: (199)
67	OTHER INFORMATION: n equals a,t,g, or c
68	NAME/KEY: misc feature
69	LOCATION: (240)
70	OTHER INFORMATION: n equals a,t,g, or c
71	NAME/KEY: misc feature
72	LOCATION: (257)
73	OTHER INFORMATION: n equals a,t,g, or c

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1 NAME/KEY: misc feature
2 LOCATION: (288)
3 OTHER INFORMATION: n equals a,t,g, or c
4 NAME/KEY: misc feature
5 LOCATION: (303)
6 OTHER INFORMATION: n equals a,t,g, or c
7 NAME/KEY: misc feature
8 LOCATION: (364)
9 OTHER INFORMATION: n equals a,t,g, or c
10 NAME/KEY: misc feature
11 LOCATION: (399)
12 OTHER INFORMATION: n equals a,t,g, or c
13 NAME/KEY: misc feature
14 LOCATION: (403)
15 OTHER INFORMATION: n equals a,t,g, or c
16 NAME/KEY: misc feature
17 LOCATION: (406)
18 OTHER INFORMATION: n equals a,t,g, or c
19 NAME/KEY: misc feature
20 LOCATION: (421)
21 OTHER INFORMATION: n equals a,t,g, or c
22 NAME/KEY: misc feature
23 LOCATION: (422)
24 OTHER INFORMATION: n equals a,t,g, or c
25 NAME/KEY: misc feature
26 LOCATION: (424)
27 OTHER INFORMATION: n equals a,t,g, or c
28 NAME/KEY: misc feature
29 LOCATION: (427)
30 OTHER INFORMATION: n equals a,t,g, or c
31 NAME/KEY: misc feature
32 LOCATION: (429)
33 OTHER INFORMATION: n equals a,t,g, or c
34 NAME/KEY: misc feature
35 LOCATION: (433)
36 OTHER INFORMATION: n equals a,t,g, or c
37 NAME/KEY: misc feature
38 LOCATION: (439)
39 OTHER INFORMATION: n equals a,t,g, or c
40 NAME/KEY: misc feature
41 LOCATION: (443)
42 OTHER INFORMATION: n equals a,t,g, or c
43 NAME/KEY: misc feature
44 LOCATION: (446)
45 OTHER INFORMATION: n equals a,t,g, or c
46 NAME/KEY: misc feature
47 LOCATION: (457)
48 OTHER INFORMATION: n equals a,t,g, or c
49 NAME/KEY: misc feature
50 LOCATION: (461)
51 OTHER INFORMATION: n equals a,t,g, or c
52 NAME/KEY: misc feature
53 LOCATION: (462)
54 OTHER INFORMATION: n equals a,t,g, or c
55 NAME/KEY: misc feature
56 LOCATION: (470)
57 OTHER INFORMATION: n equals a,t,g, or c
58 NAME/KEY: misc feature
59 LOCATION: (486)
60 OTHER INFORMATION: n equals a,t,g, or c
61 NAME/KEY: misc feature
62 LOCATION: (496)
63 OTHER INFORMATION: n equals a,t,g, or c
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: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (218)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (220)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11626

```

Query Match	22.5%;	Score 27.2;	DB 10;	Length 222;
Best Local Similarity	52.3%;	Pred. No. 3.6;		
Matches 56; Conservative	1;	Mismatches 50;	Indels 0;	Gaps 0

[illegible]

```

1 RESULT 9
2 US-09-864-761-15294
3 / Sequence 15294, Application US/09864761
4 / Patent No. US/0020048763A1
5 / GENERAL INFORMATION:
6 / APPLICANT: Penn, Sharon G.
7 / APPLICANT: Rank, David R.
8 / APPLICANT: Hanzel, David K.
9 / APPLICANT: Chen, Wensheng
10 / TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
11 / TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
12 / FILE REFERENCE: Aesomica-X-1
13 / CURRENT APPLICATION NUMBER: US/09/864,761
14 / CURRENT FILING DATE: 2001-05-23
15 / PRIOR APPLICATION NUMBER: US 60/180,312
16 / PRIOR FILING DATE: 2000-02-04
17 / PRIOR APPLICATION NUMBER: US 60/207,456
18 / PRIOR FILING DATE: 2000-05-26
19 / PRIOR APPLICATION NUMBER: US 09/632,366
20 / PRIOR FILING DATE: 2000-08-03
21 / PRIOR APPLICATION NUMBER: GB 24263. 6
22 / PRIOR FILING DATE: 2000-10-04
23 / PRIOR APPLICATION NUMBER: US 60/236,359
24 / PRIOR FILING DATE: 2000-09-27
25 / PRIOR APPLICATION NUMBER: PCT/US01/00666
26 / PRIOR FILING DATE: 2001-01-30
27 / PRIOR APPLICATION NUMBER: PCT/US01/00667
28 / PRIOR FILING DATE: 2001-01-30
29 / PRIOR APPLICATION NUMBER: PCT/US01/00664
30 / PRIOR FILING DATE: 2001-01-30
31 / PRIOR APPLICATION NUMBER: PCT/US01/00669
32 / PRIOR FILING DATE: 2001-01-30
33 / PRIOR APPLICATION NUMBER: PCT/US01/00665
34 / PRIOR FILING DATE: 2001-01-30
35 / PRIOR APPLICATION NUMBER: PCT/US01/00668
36 / PRIOR FILING DATE: 2001-01-30
37 / PRIOR APPLICATION NUMBER: PCT/US01/00663
38 / PRIOR FILING DATE: 2001-01-30
39 / PRIOR APPLICATION NUMBER: PCT/US01/00662
40 / PRIOR FILING DATE: 2001-01-30
41 / PRIOR APPLICATION NUMBER: PCT/US01/00661
42 / PRIOR FILING DATE: 2001-01-30
43 / PRIOR APPLICATION NUMBER: PCT/US01/00670
44 / PRIOR FILING DATE: 2001-01-30
45 / PRIOR APPLICATION NUMBER: US 60/234,667
46 / PRIOR FILING DATE: 2000-09-21
47 / PRIOR APPLICATION NUMBER: US 09/608,408
48 / PRIOR FILING DATE: 2000-06-30
49 / PRIOR APPLICATION NUMBER: US 09/774,203
50 / PRIOR FILING DATE: 2001-01-29
51 / NUMBER OF SEQ ID NOS: 49117

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? SOFTWARE: Anonmax Sequence Listing Engine vers. 1.1
? SEQ ID NO 15294
? LENGTH: 524
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AC024186.2
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.52
? OS 09-864 761-15234

```

Query Match	22.38;	Score 27;	DB 10;	Length 524;
Best Local Similarity	53.58;	Pred. No. 5.5;		
Matches 54;	Conservative 1;	Mismatches 46;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 10
US-09-728-952-18//C
: Sequence 18, Application US/09728952
: Patent No. US20020111302A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Zhou, Ping
: APPLICANT: Goodrich, Ryke
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Wang, Dunrui
: APPLICANT: Yamazaki, Vicki
: APPLICANT: Ujwal, Manusha L.
: APPLICANT: Dimaqac, Radaje T.
: TITLE OF INVENTION: No. US20020111302A1e1 Nucleic Acids and
: FILE REFERENCE: 799 Polypeptides
: CURRENT APPLICATION NUMBER: US/09/728,952
: CURRENT FILING DATE: 2000-11-30
: NUMBER OF SEQ ID NOS: 101
: SOFTWARE: PL_FL_genes Version 2.0
: SEQ ID NO 18
: LENGTH: 4926
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(4803)
: US-09-728-952-18

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Query Match Score 27; DB 10; length 4926;
Best Local Similarity 60.88; Pred. No. 11;
Matches 59; Conservative 1; Mismatches 36; Indels 1; Gaps 1

QY 11 TTGCTCTCTCCAGAGGCCCTCGAGTCAGTTCACGCTTTTCTCTATGGGCAATCTTAC 70
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4280 TCGATGTCCTCCAGGACAGTCCCTTGGCCGACGTCATCGCCAGGGGACACTGCGAC 4221

QY 71 TT-TGCTCCAGTTCCTGGGGCTCAGAGTCCTCGCGCC 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4220 TTGTAGCTCCATCGTGTGTGTCAAAGTCCTCCC 4184

RESULT 11
US-09-893-238-5/c
; Sequence 5, Application US/09893238
; Patient No. US20020150973A1
; GENERAL INFORMATION:

```

```
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
FILE REFERENCE: 7853-237
CURRENT FILING DATE: 2001-06-27
CURRENT APPLICATION NUMBER: US/09/893,238
PRIOR FILING DATE: 1999-07-05
PRIOR APPLICATION NUMBER: 60/093,630
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: 60/104,978
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PASTESEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 90050
TYPE: DNA
ORGANISM: Mus musculus
US-09-893-238-5
```

```
Query Match 22.1% Score 27; DB 10; Length 90050;
Best Local Similarity 57.8%; Pred. No. 29;
Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
OY 21 CAGAGCCCTCGCAGTGTGAGTTCCTTCATGCGGCAATCTYACTTTCCTTCA 80
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33058 CAGAGGACCTGGTTCATTTCTCAGACCTACGACGCTCAAGCTGTGTAATCCA 32999
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OY 81 GTTCCTGGGCTCAGAGTCCCTG 103
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Db 32998 GTCCAGGAGGATCTGATGCCAG 32976
```

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RESULT 12
US-09-789-561-57/c
Sequence 57, Application US/09789561
Patent No. US20020064818A1
```

```
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043p1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 1147
TYPE: DNA
ORGANISM: Homo sapiens
US-09-789-561-57
```

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Query Match 22.1% Score 26.8; DB 10; Length 1147;
Best Local Similarity 73.9%; Pred. No. 8.3;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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OY 71 TTTCCTTCAGTTCCTGGGCTCAGAGTCCCTTGGCCAGATGCTC 116
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 911 TTTCCTTCAGTTCCTGGGCTCAGAGTCCCTTGGCTGATGCTC 866
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RESULT 13
US-09-764-864-1714/c
Sequence 1714, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Fosen et al.
```

```
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1714
LENGTH: 15980
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2577)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-1714
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Query Match 22.1% Score 26.8; DB 10; Length 15980;
Best Local Similarity 59.7%; Pred. No. 19;
Matches 43; Conservative 1; Mismatches 28; Indels 0; Gaps 0;
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OY 40 GTTCAGCTTTCTCATGAGGCAATCTYACTTTCCTTCAGTTCCTGGGCTCAGAGTC 99
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1077 GTTCAGCTTTCTTCCTGCGGCGCTTTCCTGCTCAGCTTCTTCGCGGCGGCT 1018
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 100 CCGGCGCCAGAT 111
||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1017 CCCAGCCAGAT 1006
```

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RESULT 14
US-09-864-761-5516/c
Sequence 5516, Application US/09864761
Patent No. US20020048763A1
```

```
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenshang
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecomic-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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1 PRIOR FILING DATE: 2001-01-30
2 PRIOR APPLICATION NUMBER: US 60/234,687
3 PRIOR FILING DATE: 2000-09-21
4 PRIOR APPLICATION NUMBER: US 09/608,408
5 PRIOR FILING DATE: 2000-06-30
6 PRIOR APPLICATION NUMBER: US 09/774,203
7 PRIOR FILING DATE: 2001-01-29
8 NUMBER OF SEQ ID NOS: 49117
9 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
10 SEQ ID NO 5516
11 LENGTH: 472
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 FEATURE:
15 OTHER INFORMATION: MAP TO AC004613.1
16 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 2.2
17 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 1.7
18 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2
19 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL 1.8
20 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 2
21 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.7
22 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 1.6
23 US-09-864-761-5516

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Query Match	22.08;	Score 26.6;	DB 10;	Length 472;
Best Local Similarity	64.48;	Pred. No. 7.2;		
Matches 38; Conservative	1;	Mismatches 20;	Indels 0;	Gaps 0;

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Qy      55  ATGGGCAATCTYACTTTCGCTCCAGTTCCTGGGCTCAGAGTCCCTGGCCACAATGC 113
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      302  AAGGGCAAGCTCAGTTTCACCTGCACTAAATGACGCACATATGGGCTTGCAACAAGTTTC 244

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RESULT 15
US-09-917-800A-61/C

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1 Sequence bl, Application US/0991/800A
2 Patent No. US2002119462A1
3
4 GENERAL INFORMATION:
5 APPLICANT: Mendrick, Donna
6 APPLICANT: Porter, Mark
7 APPLICANT: Johnson, Kory
8 APPLICANT: Castle, Arthur
9 APPLICANT: Elashoff, Michael
10 APPLICANT: Gene Logic, Inc.
11
12 TITLE OF INVENTION: Molecular Toxicology Modeling
13
14 CURRENT REFERENCE: 44921-5038-US
15 CURRENT APPLICATION NUMBER: US/09/917,800A
16
17 CURRENT FILING DATE: 2001-07-31
18
19 PRIOR APPLICATION NUMBER: US 60/222,040
20
21 PRIOR FILING DATE: 2000-07-31
22
23 PRIOR APPLICATION NUMBER: US 60/222,080
24
25 PRIOR FILING DATE: 2000-11-02
26
27 PRIOR APPLICATION NUMBER: US 60/290,029
28
29 PRIOR FILING DATE: 2001-05-11
30
31 PRIOR APPLICATION NUMBER: US 60/290,045
32
33 PRIOR FILING DATE: 2001-05-15
34
35 PRIOR APPLICATION NUMBER: US 60/292,336
36
37 PRIOR FILING DATE: 2001-05-22
38
39 PRIOR APPLICATION NUMBER: US 60/295,798
40
41 PRIOR FILING DATE: 2001-06-06
42
43 PRIOR APPLICATION NUMBER: US 60/297,457
44
45 PRIOR FILING DATE: 2001-06-13
46
47 PRIOR APPLICATION NUMBER: US 60/298,884
48
49 PRIOR FILING DATE: 2001-06-19
50
51 PRIOR APPLICATION NUMBER: US 60/303,459
52
53 PRIOR FILING DATE: 2001-07-09
54
55 NUMBER OF SEQ ID NOS: 1740
56
57 SOFTWARE: PatentIn Ver. 2.1
58
59 SEQ ID NO: 61
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61 LENGTH: 494
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63 TYPE: DNA
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65 ORGANISM: Rattus norvegicus

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; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA818264
US-09-917-800A-61

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Query Match	22.0%	Score 26.6	DB 10	Length 494
Best Local Similarity	53.3%	Pred. No. 7.3		
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 Db 193 CATTGTTCTTCCATATGTTTGTGGACAACATGTGGACACTGCTTTCTTTGGGAGACCCGA 134

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Oy      70 CTTTCGCTCCAGTCTCCTGGGGCTCAGACTCCCTGCCCCAGATGCC 114
          || || || || || || || || || || || || || || || ||
Db     133 CTATTCCTGCAGTCCCTGTGGCCGACATCCTTACCCAGAGACC 89

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Job time : 134 secs